

1647

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1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/830,972

DATE: 11/04/2002

TIME: 13:39:14

Input Set : A:\10200-003.txt

Output Set: N:\CRF4\11042002\I830972.raw

4 <110> APPLICANT: Schwab, M.
5 Chen, M.
7 <120> TITLE OF INVENTION: NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO
8 GENES AND METHODS BASED THEREON
11 <130> FILE REFERENCE: 10200-003-999
13 <140> CURRENT APPLICATION NUMBER: 09/830,972
14 <141> CURRENT FILING DATE: 2001-09-24
16 <150> PRIOR APPLICATION NUMBER: PCT/US99/26160
17 <151> PRIOR FILING DATE: 1999-11-05
19 <150> PRIOR APPLICATION NUMBER: 60/107,446
20 <151> PRIOR FILING DATE: 1998-11-06
22 <160> NUMBER OF SEQ ID NOS: 51
24 <170> SOFTWARE: FastSEQ for Windows Version 3.0
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 3741
28 <212> TYPE: DNA
29 <213> ORGANISM: Rattus sp.
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (253)...(3741)
35 <400> SEQUENCE: 1
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37 atcgcggaagg cagcagaagc agtctcattg ttccgggagc cgtcgccctct gcaggttctt 120
38 cggctcgggt cggcacgact cggcctgcct ggccctgcc agtcttgccc aacccccaca 180
39 accgcccgcg actctgagga gaagcggccc tgcggcggct gtagctgcag catcgtcggc 240
40 gaccgcgcag cc atg gaa gac ata gac cag tcg tcg ctg gtc tcc tcg tcc 291
41 Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser
42 1 5 10
44 acg gac agc ccg ccc cgg cct ccg ccc gcc ttc aag tac cag ttc gtg 339
45 Thr Asp Ser Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val
46 15 20 25
48 acg gag ccc gag gac gag gag gag gag gag gag gag gag gag gag 387
49 Thr Glu Pro Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu
50 30 35 40 45
52 gag gac gac gag gac cta gag gaa ctg gag gtg ctg gag agg aag ccc 435
53 Glu Asp Asp Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro
54 50 55 60
56 gca gcc ggg ctg tcc gca gct gcg gtg ccg ccc gcc gcc gcc gcg ccg 483
57 Ala Ala Gly Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Ala Pro
58 65 70 75
59 ctg ctg gac ttc agc agc gac tcg gtg ccc ccc gcg ccc cgc ggg ccg 531
60 Leu Leu Asp Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro
61 80 85 90

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63	ctg ccg gcc gcg ccc cct gcc gct cct gag agg cag cca tcc tgg gaa	579
64	Leu Pro Ala Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu	
65	95 100 105	
67	cgc agc ccc gcg gcg ccc gcg cca tcc ctg ccg ccc gct gcc gca gtc	627
68	Arg Ser Pro Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val	
69	110 115 120 125	
71	ctg ccc tcc aag ctc cca gag gac gac gag cct ccg gcg agg ccc ccg	675
72	Leu Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro	
73	130 135 140	
75	cct ccg ccg cca gcc ggc gcg agc ccc ctg gcg gag ccc gcc gcg ccc	723
76	Pro Pro Pro Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro	
77	145 150 155	
79	cct tcc acg ccg gcc gcg ccc aag cgc agg ggc tcc ggc tca gtg gat	771
80	Pro Ser Thr Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp	
81	160 165 170	
83	gag acc ctt ttt gct ctt cct gct gca tct gag cct gtg ata ccc tcc	819
84	Glu Thr Leu Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser	
85	175 180 185	
87	tct gca gaa aaa att atg gat ttg atg gag cag cca ggt aac act gtt	867
88	Ser Ala Glu Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val	
89	190 195 200 205	
91	tcg tct ggt caa gag gat ttc cca tct gtc ctg ctt gaa act gct gcc	915
92	Ser Ser Gly Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala	
93	210 215 220	
95	tct ctt cct tct cta tct cct ctc tca act gtt tct ttt aaa gaa cat	963
96	Ser Leu Pro Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His	
97	225 230 235	
99	gga tac ctt ggt aac tta tca gca gtg tca tcc tca gaa gga aca att	1011
100	Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile	
101	240 245 250	
103	gaa gaa act tta aat gaa gct tct aaa gag ttg cca gag agg gca aca	1059
104	Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr	
105	255 260 265	
107	aat cca ttt gta aat aga gat tta gca gaa ttt tca gaa tta gaa tat	1107
108	Asn Pro Phe Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr	
109	270 275 280 285	
111	tca gaa atg gga tca tct ttt aaa ggc tcc cca aaa gga gag tca gcc	1155
112	Ser Glu Met Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala	
113	290 295 300	
114	ata tta gta gaa aac act aag gaa gaa gta att gtg agg agt aaa gac	1203
115	Ile Leu Val Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp	
116	305 310 315	
118	aaa gag gat tta gtt tgt agt gca gcc ctt cac agt cca caa gaa tca	1251
119	Lys Glu Asp Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser	
120	320 325 330	
122	cct gtg ggt aaa gaa gac aga gtt gtg tct cca gaa aag aca atg gac	1299
123	Pro Val Gly Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp	
124	335 340 345	
126	att ttt aat gaa atg cag atg tca gta gta gca cct gtg agg gaa gag	1347

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127	Ile	Phe	Asn	Glu	Met	Gln	Met	Ser	Val	Val	Ala	Pro	Val	Arg	Glu	Glu	
128	350					355					360					365	
130	tat	gca	gac	ttt	aag	cca	ttt	gaa	caa	gca	tgg	gaa	gtg	aaa	gat	act	1395
131	Tyr	Ala	Asp	Phe	Lys	Pro	Phe	Glu	Gln	Ala	Trp	Glu	Val	Lys	Asp	Thr	
132					370					375					380		
134	tat	gag	gga	agt	agg	gat	gtg	ctg	gct	aga	gct	aat	gtg	gaa	agt		1443
135	Tyr	Glu	Gly	Ser	Arg	Asp	Val	Leu	Ala	Ala	Arg	Ala	Asn	Val	Glu	Ser	
136					385				390					395			
138	aaa	gtg	gac	aga	aaa	tgc	ttg	gaa	gat	agc	ctg	gag	caa	aaa	agt	ctt	1491
139	Lys	Val	Asp	Arg	Lys	Cys	Leu	Glu	Asp	Ser	Leu	Glu	Gln	Lys	Ser	Leu	
140					400				405					410			
142	ggg	aag	gat	agt	gaa	ggc	aga	aat	gag	gat	gct	tct	ttc	ccc	agt	acc	1539
143	Gly	Lys	Asp	Ser	Glu	Gly	Arg	Asn	Glu	Asp	Ala	Ser	Phe	Pro	Ser	Thr	
144					415				420					425			
146	cca	gaa	cct	gtg	aag	gac	agc	tcc	aga	gca	tat	att	acc	tgt	gct	tcc	1587
147	Pro	Glu	Pro	Val	Lys	Asp	Ser	Ser	Arg	Ala	Tyr	Ile	Thr	Cys	Ala	Ser	
148	430					435					440					445	
150	ttt	acc	tca	gca	acc	gaa	agc	acc	aca	gca	aac	act	ttc	cct	ttg	tta	1635
151	Phe	Thr	Ser	Ala	Thr	Glu	Ser	Thr	Thr	Ala	Asn	Thr	Phe	Pro	Leu	Leu	
152					450						455					460	
154	gaa	gat	cat	act	tca	gaa	aat	aaa	aca	gat	gaa	aaa	aaa	ata	gaa	gaa	1683
155	Glu	Asp	His	Thr	Ser	Glu	Asn	Lys	Thr	Asp	Glu	Lys	Lys	Ile	Glu	Glu	
156					465					470						475	
158	agg	aag	gcc	caa	att	ata	aca	gag	aag	act	agc	ccc	aaa	acg	tca	aat	1731
159	Arg	Lys	Ala	Gln	Ile	Ile	Thr	Glu	Lys	Thr	Ser	Pro	Lys	Thr	Ser	Asn	
160					480				485					490			
162	cct	ttc	ctt	gta	gca	gta	cag	gat	tct	gag	gca	gat	tat	gtt	aca	aca	1779
163	Pro	Phe	Leu	Val	Ala	Val	Gln	Asp	Ser	Glu	Ala	Asp	Tyr	Val	Thr	Thr	
164					495				500					505			
166	gat	acc	tta	tca	aag	gtg	act	gag	gca	gca	gtg	tca	aac	atg	cct	gaa	1827
167	Asp	Thr	Leu	Ser	Lys	Val	Thr	Glu	Ala	Ala	Val	Ser	Asn	Met	Pro	Glu	
168	510					515					520					525	
169	ggt	ctg	acg	cca	gat	tta	gtt	cag	gaa	gca	tgt	gaa	agt	gaa	ctg	aat	1875
170	Gly	Leu	Thr	Pro	Asp	Leu	Val	Gln	Glu	Ala	Cys	Glu	Ser	Glu	Leu	Asn	
171					530						535					540	
173	gaa	gcc	aca	ggt	aca	aag	att	gct	tat	gaa	aca	aaa	gtg	gac	ttg	gtc	1923
174	Glu	Ala	Thr	Gly	Thr	Lys	Ile	Ala	Tyr	Glu	Thr	Lys	Val	Asp	Leu	Val	
175					545					550						555	
177	caa	aca	tca	gaa	gct	ata	caa	gaa	tca	ctt	tac	ccc	aca	gca	cag	ctt	1971
178	Gln	Thr	Ser	Glu	Ala	Ile	Gln	Glu	Ser	Leu	Tyr	Pro	Thr	Ala	Gln	Leu	
179					560					565						570	
181	tgc	cca	tca	ttt	gag	gaa	gct	gaa	gca	act	ccg	tca	cca	gtt	ttg	cct	2019
182	Cys	Pro	Ser	Phe	Glu	Glu	Ala	Glu	Ala	Thr	Pro	Ser	Pro	Val	Leu	Pro	
183					575				580					585			
185	gat	att	gtt	atg	gaa	gca	cca	tta	aat	tct	ctc	ctt	cca	agc	gct	ggt	2067
186	Asp	Ile	Val	Met	Glu	Ala	Pro	Leu	Asn	Ser	Leu	Leu	Pro	Ser	Ala	Gly	
187	590					595					600					605	
189	gct	tct	gta	gtg	cag	ccc	agt	gta	tcc	cca	ctg	gaa	gca	cct	cct	cca	2115
190	Ala	Ser	Val	Val	Gln	Pro	Ser	Val	Ser	Pro	Leu	Glu	Ala	Pro	Pro	Pro	

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191				610				615				620					
193	gtt	agt	tat	gac	agt	ata	aag	ctt	gag	cct	gaa	aac	ccc	cca	cca	tat	2163
194	Val	Ser	Tyr	Asp	Ser	Ile	Lys	Leu	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	
195				625				630				635					
197	gaa	gaa	gcc	atg	aat	gta	gca	cta	aaa	gct	ttg	gga	aca	aag	gaa	gga	2211
198	Glu	Glu	Ala	Met	Asn	Val	Ala	Leu	Lys	Ala	Leu	Gly	Thr	Lys	Glu	Gly	
199			640					645				650					
201	ata	aaa	gag	cct	gaa	agt	ttt	aat	gca	gct	gtt	cag	gaa	aca	gaa	gct	2259
202	Ile	Lys	Glu	Pro	Glu	Ser	Phe	Asn	Ala	Ala	Val	Gln	Glu	Thr	Glu	Ala	
203		655					660				665						
205	cct	tat	ata	tcc	att	gcg	tgt	gat	tta	att	aaa	gaa	aca	aag	ctc	tcc	2307
206	Pro	Tyr	Ile	Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu	Ser	
207	670					675			680			685					
209	act	gag	cca	agt	cca	gat	ttc	tct	aat	tat	tca	gaa	ata	gca	aaa	ttc	2355
210	Thr	Glu	Pro	Ser	Pro	Asp	Phe	Ser	Asn	Tyr	Ser	Glu	Ile	Ala	Lys	Phe	
211			690					695			700						
213	gag	aag	tcg	gtg	ccc	gaa	cac	gct	gag	cta	gtg	gag	gat	tcc	tca	cct	2403
214	Glu	Lys	Ser	Val	Pro	Glu	His	Ala	Glu	Leu	Val	Glu	Asp	Ser	Ser	Pro	
215			705					710			715						
217	gaa	tct	gaa	cca	gtt	gac	tta	ttt	agt	gat	gat	tcg	att	cct	gaa	gtc	2451
218	Glu	Ser	Glu	Pro	Val	Asp	Leu	Phe	Ser	Asp	Asp	Ser	Ile	Pro	Glu	Val	
219			720					725			730						
221	cca	caa	aca	caa	gag	gag	gct	gtg	atg	ctc	atg	aag	gag	agt	ctc	act	2499
222	Pro	Gln	Thr	Gln	Glu	Glu	Ala	Val	Met	Leu	Met	Lys	Glu	Ser	Leu	Thr	
223		735					740				745						
225	gaa	gtg	tct	gag	aca	gta	gcc	cag	cac	aaa	gag	gag	aga	ctt	agt	gcc	2547
226	Glu	Val	Ser	Glu	Thr	Val	Ala	Gln	His	Lys	Glu	Glu	Arg	Leu	Ser	Ala	
227	750					755			760			765					
229	tca	cct	cag	gag	cta	gga	aag	cca	tat	tta	gag	tct	ttt	cag	ccc	aat	2595
230	Ser	Pro	Gln	Glu	Leu	Gly	Lys	Pro	Tyr	Leu	Glu	Ser	Phe	Gln	Pro	Asn	
231			770					775			780						
233	tta	cat	agt	aca	aaa	gat	gct	gca	tct	aat	gac	att	cca	aca	ttg	acc	2643
234	Leu	His	Ser	Thr	Lys	Asp	Ala	Ala	Ser	Asn	Asp	Ile	Pro	Thr	Leu	Thr	
235			785					790			795						
237	aaa	aag	gag	aaa	att	tct	ttg	caa	atg	gaa	gag	ttt	aat	act	gca	att	2691
238	Lys	Lys	Glu	Lys	Ile	Ser	Leu	Gln	Met	Glu	Glu	Phe	Asn	Thr	Ala	Ile	
239		800					805				810						
241	tat	tca	aat	gat	gac	tta	ctt	tct	tct	aag	gaa	gac	aaa	ata	aaa	gaa	2739
242	Tyr	Ser	Asn	Asp	Asp	Leu	Leu	Ser	Ser	Lys	Glu	Asp	Lys	Ile	Lys	Glu	
243		815					820				825						
245	agt	gaa	aca	ttt	tca	gat	tca	tct	ccg	att	gag	ata	ata	gat	gaa	ttt	2787
246	Ser	Glu	Thr	Phe	Ser	Asp	Ser	Ser	Pro	Ile	Glu	Ile	Ile	Asp	Glu	Phe	
247	830					835			840			845					
249	ccc	acg	ttt	gtc	agt	gct	aaa	gat	gat	tct	cct	aaa	tta	gcc	aag	gag	2835
250	Pro	Thr	Phe	Val	Ser	Ala	Lys	Asp	Asp	Ser	Pro	Lys	Leu	Ala	Lys	Glu	
251			850					855			860						
253	tac	act	gat	cta	gaa	gta	tcc	gac	aaa	agt	gaa	att	gct	aat	atc	caa	2883
254	Tyr	Thr	Asp	Leu	Glu	Val	Ser	Asp	Lys	Ser	Glu	Ile	Ala	Asn	Ile	Gln	
255			865					870			875						

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257	agc ggg gca gat tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct	2931
258	Ser Gly Ala Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser	
259	880 885 890	
261	ttc aag aat ata tat cct aaa gat gaa gta cat gtt tca gat gaa ttc	2979
262	Phe Lys Asn Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe	
263	895 900 905	
265	tcc gaa aat agg tcc agt gta tct aag gca tcc ata tcg cct tca aat	3027
266	Ser Glu Asn Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn	
267	910 915 920 925	
269	gtc tct gct ttg gaa cct cag aca gaa atg ggc agc ata gtt aaa tcc	3075
270	Val Ser Ala Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser	
271	930 935 940	
273	aaa tca ctt acg aaa gaa gca gag aaa aaa ctt cct tct gac aca gag	3123
274	Lys Ser Leu Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu	
275	945 950 955	
277	aaa gag gac aga tcc ctg tca gct gta ttg tca gca gag ctg agt aaa	3171
278	Lys Glu Asp Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys	
279	960 965 970	
281	act tca gtt gtt gac ctc ctc tac tgg aga gac att aag aag act gga	3219
282	Thr Ser Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly	
283	975 980 985	
285	gtg gtg ttt ggt gcc agc tta ttc ctg ctg ctg tct ctg aca gtg ttc	3267
286	Val Val Phe Gly Ala Ser Leu Phe Leu Leu Ser Leu Thr Val Phe	
287	990 995 1000 1005	
289	agc att gtc agt gta acg gcc tac att gcc ttg gcc ctg ctc tcg gtg	3315
290	Ser Ile Val Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val	
291	1010 1015 1020	
293	act atc agc ttt agg ata tat aag ggc gtg atc cag gct atc cag aaa	3363
294	Thr Ile Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys	
295	1025 1030 1035	
297	tca gat gaa ggc cac cca ttc agg gca tat tta gaa tct gaa gtt gct	3411
298	Ser Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala	
299	1040 1045 1050	
301	ata tca gag gaa ttg gtt cag aaa tac agt aat tct gct ctt ggt cat	3459
302	Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His	
303	1055 1060 1065	
305	gtg aac agc aca ata aaa gaa ctg agg cgg ctt ttc tta gtt gat gat	3507
306	Val Asn Ser Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp	
307	1070 1075 1080 1085	
309	tta gtt gat tcc ctg aag ttt gca gtg ttg atg tgg gtg ttt act tat	3555
310	Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr	
311	1090 1095 1100	
313	gtt ggt gcc ttg ttc aat ggt ctg aca cta ctg att tta gct ctg atc	3603
314	Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile	
315	1105 1110 1115	
317	tca ctc ttc agt att cct gtt att tat gaa cgg cat cag gtg cag ata	3651
318	Ser Leu Phe Ser Ile Pro Val Ile Tyr Glu Arg His Gln Val Gln Ile	
319	1120 1125 1130	
321	gat cat tat cta gga ctt gca aac aag agt gtt aag gat gcc atg gcc	3699

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 2
Seq#:6; Xaa Pos. 2,5
Seq#:29; Xaa Pos. 187,188,189,190,221,328,477
Seq#:30; Xaa Pos. 469
Seq#:35; N Pos. 110
Seq#:36; N Pos. 91
Seq#:37; N Pos. 170,275
Seq#:38; N Pos. 371,444,474,501,506,524,544,561,580,614,620
Seq#:39; N Pos. 149,198,207,246,312,317
Seq#:42; N Pos. 383,402,421,433,441
Seq#:47; N Pos. 3,6,12,15,18
Seq#:48; N Pos. 3,6,9,12,15
Seq#:49; N Pos. 3,6,12,15,20
Seq#:50; N Pos. 3,6,9,12,15,18,21
Seq#:51; N Pos. 9,12,24